sequence having at least 95% homology to SEQ ID NO:1, with an amino acid sequence from 1st His to 21st Gly of SEQ ID NO:2, wherein said mutant α-amylase possess increased heat resistance and maintains resistance to chelating agents when compared to SEQ ID NO:1.

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5. (Three Times Amended) A mutant α-amylase obtained by introducing a first mutation and a second mutation into SEQ ID NO:1 or an amino acid sequence having at least 95% homology to SEQ ID NO:1,

wherein said first mutation consists of a substitution or a deletion of at least one amino acid residue selected from the group consisting of the 11th Tyr, 16th Glu, 49th Asn, 84th Glu, 144th Ser, 167th Gln, 169th Tyr, 178th Ala, 188th Glu, 190th Asn, 205th His and 209th Gln, and

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wherein said second mutation consists of a substitution of a sequence corresponding to the 11th to 100th amino acid residue from the amino terminus of the amino acid sequence set forth in SEQ ID NO:1, and

wherein said mutant α-amylase possesses increased heat resistance and maintains resistance to chelating agents when compared to SEQ ID NO:1.

6. (Twice Amended) The mutant α-amylase according to Claim 5, wherein said first mutation consists of:

the substitution of an amino acid residue selected from the group consisting of: the 11th Tyr of SEQ ID NO:1 with Phe, the 16th Glu of SEQ ID NO:1 with Pro, the 49th Asn of SEQ ID NO:1 with Ser, the 167 Gln of SEQ ID NO:1 with Glu, the 169th Tyr of SEQ ID NO:1 with Lys, the 190th Asn of SEQ ID NO:1 with Phe, the 205th His of SEQ ID NO:1 with Arg, and the 209th Gln of SEQ ID NO:1 with Val,

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and wherein said second mutation consists of:

substituting an amino terminal sequence from 1st Asp through 19th Gly of SEQ ID NO:1 with an amino acid sequence from 1st His to 21st Gly of SEQ ID NO:2.

13. (Amended) A mutant α-amylase obtained by making a substitution or deletion of at least one amino acid residue of specific positions in SEQ ID NO:1, or by making a substitution or deletion of at least one amino acid residue corresponding to the above-mentioned amino acid residue in a sequence having at least 95% homology to SEQ ID NO:1,

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wherein said at least one amino acid residue is selected from the group consisting of:

the 11th Tyr, 16th Glu, 49th Asn, 84th Glu, 144th Ser, 167th Gln, 169th Tyr, 178th Ala, 188th Glu, 190th Asn, 205th His and 209th Gln, and

wherein said mutant α-amylase:

(i) decomposes α-1,4-glycoside bonds of starch, amylose, amylopectin, and partially decomposed products thereof;

(ii) produces glucose, maltose, maltotriose, maltotetraose, maltopentaose, maltohexaose, and maltoheptaose from amylose;

(iii) does not act on pullulan;

(iv) exhibits a residual activity of at least 70% in a pH range of 6.5 to 11 under treatment conditions of 40°C and 30 minutes;

(v) acts in a temperature range of 20°C to 80°C;

(vi) exhibits a residual activity of at least 80% when incubated at 40°C, or at least 60% when incubated at 45°C, for 30 minutes in 50 mM glycine-sodium hydroxide buffer at pH 10;

(vii) has a molecular weight of 55,000 ± 5,000 as measured by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis;

(viii) has an isoelectric point of about 4.2 as measured by isoelectric focusing;

(ix) has a residual activity of at least 90% when treated at pH 10 and 30^{0}C for 30 minutes in a 0.1% solution of a surfactant selected from the group consisting of:

sodium linear alkylbenzenesulfonates, sodium alkylsulfates, sodium polyoxyethylene alkylsulfates, sodium α-olefinsulfonates, sodium salts of α-sulfonated fatty acid esters, sodium alkylsulfonates, SDS, soap, and Softanol;

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(x) is inhibited by 1 mM Mn^{2+} by about 75%, or by 1 mM Sr^{2+} or 1 mM Cd^{2+} by about 30 to 40%, when treated at pH 10 and 30^{0}C for 30 minutes; and

(xii) comprises an amino acid sequence which is at least 70% homologous to SEQ ID NO:1.

Please add the following claims:

--15. The mutant α-amylase according to claim 12, wherein the 11th Tyr of SEQ ID NO:1 is substituted with Phe, the 16th Glu of SEQ ID NO:1 is substituted with Pro, the 49th Asn of SEQ ID NO:1 is substituted with Ser, the 167 Gln of SEQ ID NO:1 is substituted with Glu, the 169th Tyr of SEQ ID NO:1 is substituted with Lys, the 190th Asn of SEQ ID NO:1 is substituted with Phe,

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the 205th His of SEQ ID NO:1 is substituted with Arg, and the 209th Gln of SEQ ID NO:1 is substituted with Val.--

--16. The mutant α-amylase according to claim 13, wherein said mutant α-amylase comprises an amino acid sequence which is at least 95% homologous to SEQ ID NO:1.--

--17. The mutant α-amylase according to claim 13 or 16, wherein the 11th Tyr of SEQ ID NO:1 is replaced with Phe.--

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--18. The mutant α-amylase according to claim 13 or 16, wherein the 16th Glu of SEQ ID NO:1 is replaced with Pro.--

--19. The mutant α-amylase according to claim 13 or 16, wherein the 49th Asn of SEQ ID NO:1 is replaced with Ser.--

--20. The mutant α-amylase according to claim 13 or 16, wherein the 167 Gln of SEQ ID NO:1 is replaced with Glu.--

--21. The mutant α-amylase according to claim 13 or 16, wherein the 169th Tyr of SEQ ID NO:1 is replaced with Lys.--

--22. The mutant α-amylase according to claim 13 or 16, wherein the 190th Asn of SEQ ID NO:1 is replaced with Phe.--

--23. The mutant α-amylase according to claim 13 or 16, wherein the 205th His of SEQ ID NO:1 is replaced with Arg.--

--24. The mutant α-amylase according to claim 13 or 16, wherein the 209th Gln of SEQ ID NO:1 is replaced with Val.--

--25. A mutant α-amylase obtained by introducing a mutation into SEQ ID NO:1,

75 wherein said mutation consists of:

the substitution of an amino acid residue selected from the group consisting of: the 11th Tyr, 16th Glu, 49th Asn, 84th Glu, 144th Ser, 167th Gln, 169th Tyr, 178th Ala, 188th Glu, 190th Asn, 205th His and 209th Gln, with another amino acid.--

--26. The mutant α-amylase according to claim 25, wherein the 11th Tyr of SEQ ID NO:1 is substituted with Phe, the 16th Glu of SEQ ID NO:1 is substituted with Pro, the 49th Asn of SEQ ID NO:1 is substituted with Ser, the 167 Gln of SEQ ID NO:1 is substituted with Glu, the 169th Tyr of SEQ ID NO:1 is substituted with Lys, the 190th Asn of SEQ ID NO:1 is substituted with Phe,

the 205th His of SEQ ID NO:1 is substituted with Arg, and the 209th Gln of SEQ ID NO:1 is substituted with Val.—

--27. A mutant α-amylase obtained by introducing a mutation into SEQ ID NO:1,

75 and wherein said mutation consists of:

substituting an amino terminal sequence from 1st Asp through 19th Gly of SEQ ID NO:1 with an amino acid sequence from 1st His to 21st Gly of SEQ ID NO:2.--

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Attached hereto is a marked-up version showing the changes made to the application by this Reply.